Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED   CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 ✓ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) ___7___. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 ✓ Use of <220>Feature (NEW RULES)
Sequence(s) #7 are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING   DATE: 08/23/2000
PATENT APPLICATION: US/09/637,302   TIME: 09:32:54

Input Set : A:\TSR7102.txt
Output Set: N:\CRF3\08232000\I637302.raw

```
   3 <110> APPLICANT: HOOD, John
   4         ELICEIRI, Brian
   5         CHERESH, David
   7 <120> TITLE OF INVENTION: Methods and Compositions Useful for Modulation of
   8         Angiogenesis Using Tyrosine Kinase Raf and Ras
  10 <130> FILE REFERENCE: TSRI 710.2
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/637,302
C--> 13 <141> CURRENT FILING DATE: 2000-08-11
  15 <150> PRIOR APPLICATION NUMBER: US 60/148,924
  16 <151> PRIOR FILING DATE: 1999-08-13
  18 <150> PRIOR APPLICATION NUMBER: US 60/215,951
  19 <151> PRIOR FILING DATE: 2000-07-05
  21 <160> NUMBER OF SEQ ID NOS: 7
  23 <170> SOFTWARE: PatentIn Ver. 2.0
  25 <210> SEQ ID NO: 1
  26 <211> LENGTH: 2977
  27 <212> TYPE: DNA
  28 <213> ORGANISM: Homo sapiens
  30 <220> FEATURE:
  31 <221> NAME/KEY: CDS
  32 <222> LOCATION: (130)..(2073)
  34 <400> SEQUENCE: 1
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  37   tgccgccgaa cgacaggacg ttggggcggc ctggctccct caggtttaag aattgtttaa 120
  39   gctgcatca atg gag cac ata cag gga gct tgg aag acg atc agc aat ggt 171
  40              Met Glu His Ile Gln Gly Ala Trp Lys Thr Ile Ser Asn Gly
  41               1               5                  10
  43   ttt gga ttc aaa gat gcc gtg ttt gat ggc tcc agc tgc atc tct cct   219
  44   Phe Gly Phe Lys Asp Ala Val Phe Asp Gly Ser Ser Cys Ile Ser Pro
  45    15              20                  25                  30
  47   aca ata gtt cag cag ttt ggc tat cag cgc cgg gca tca gat gat ggc   267
  48   Thr Ile Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly
  49                   35                  40                  45
  51   aaa ctc aca gat cct tct aag aca agc aac act atc cgt gtt ttc ttg   315
  52   Lys Leu Thr Asp Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu
  53               50                  55                  60
  55   ccg aac aag caa aga aca gtg gtc aat gtg cga aat gga atg agc ttg   363
  56   Pro Asn Lys Gln Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu
  57           65                  70                  75
  59   cat gac tgc ctt atg aaa gca ctc aag gtg agg ggc ctg caa cca gag   411
  60   His Asp Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu
  61       80                  85                  90
  63   tgc tgt gca gtg ttc aga ctt ctc cac gaa cac aaa ggt aaa aaa gca   459
  64   Cys Cys Ala Val Phe Arg Leu Leu His Glu His Lys Gly Lys Lys Ala
  65    95                  100                 105                 110
  67   cgc tta gat tgg aat act gat gct gcg tct ttg att gga gaa gaa ctt   507
  68   Arg Leu Asp Trp Asn Thr Asp Ala Ala Ser Leu Ile Gly Glu Glu Leu
```

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                    RAW SEQUENCE LISTING            DATE: 08/23/2000
                    PATENT APPLICATION:  US/09/637,302   TIME: 09:32:54

                    Input Set : A:\TSR7102.txt
                    Output Set: N:\CRF3\08232000\I637302.raw

69                    115               120               125
71  caa gta gat ttc ctg gat cat gtt ccc ctc aca aca cac aac ttt gct   555
72  Gln Val Asp Phe Leu Asp His Val Pro Leu Thr Thr His Asn Phe Ala
73                130               135               140
75  cgg aag acg ttc ctg aag ctt gcc ttc tgt gac atc tgt cag aaa ttc   603
76  Arg Lys Thr Phe Leu Lys Leu Ala Phe Cys Asp Ile Cys Gln Lys Phe
77            145               150               155
79  ctg ctc aat gga ttt cga tgt cag act tgt ggc tac aaa ttt cat gag   651
80  Leu Leu Asn Gly Phe Arg Cys Gln Thr Cys Gly Tyr Lys Phe His Glu
81        160               165               170
83  cac tgt agc acc aaa gta cct act atg tgt gtg gac tgg agt aac atc   699
84  His Cys Ser Thr Lys Val Pro Thr Met Cys Val Asp Trp Ser Asn Ile
85  175               180               185               190
87  aga caa ctc tta ttg ttt cca aat tcc act att ggt gat agt gga gtc   747
88  Arg Gln Leu Leu Leu Phe Pro Asn Ser Thr Ile Gly Asp Ser Gly Val
89                195               200               205
91  cca gca cta cct tct ttg act atg cgt cgt atg cga gag tct gtt tcc   795
92  Pro Ala Leu Pro Ser Leu Thr Met Arg Arg Met Arg Glu Ser Val Ser
93            210               215               220
95  agg atg cct gtt agt tct cag cac aga tat tct aca cct cac gcc ttc   843
96  Arg Met Pro Val Ser Ser Gln His Arg Tyr Ser Thr Pro His Ala Phe
97        225               230               235
99  acc ttt aac acc tcc agt ccc tca tct gaa ggt tcc ctc tcc cag agg   891
100 Thr Phe Asn Thr Ser Ser Pro Ser Ser Glu Gly Ser Leu Ser Gln Arg
101     240               245               250
103 cag agg tcg aca tcc aca cct aat gtc cac atg gtc agc acc acg ctg   939
104 Gln Arg Ser Thr Ser Thr Pro Asn Val His Met Val Ser Thr Thr Leu
105 255               260               265               270
107 cct gtg gac agc agg atg att gag gat gca att cga agt cac agc gaa   987
108 Pro Val Asp Ser Arg Met Ile Glu Asp Ala Ile Arg Ser His Ser Glu
109                275               280               285
111 tca gcc tca cct tca gcc ctg tcc agt agc ccc aac aat ctg agc cca   1035
112 Ser Ala Ser Pro Ser Ala Leu Ser Ser Ser Pro Asn Asn Leu Ser Pro
113                290               295               300
115 aca ggc tgg tca cag ccg aaa acc ccc gtg cca gca caa aga gag cgg   1083
116 Thr Gly Trp Ser Gln Pro Lys Thr Pro Val Pro Ala Gln Arg Glu Arg
117            305               310               315
119 gca cca gta tct ggg acc cag gag aaa aac aaa att agg cct cgt gga   1131
120 Ala Pro Val Ser Gly Thr Gln Glu Lys Asn Lys Ile Arg Pro Arg Gly
121     320               325               330
123 cag aga gat tca agc tat tat tgg gaa ata gaa gcc agt gaa gtg atg   1179
124 Gln Arg Asp Ser Ser Tyr Tyr Trp Glu Ile Glu Ala Ser Glu Val Met
125 335               340               345               350
127 ctg tcc act cgg att ggg tca ggc tct ttt gga act gtt tat aag ggt   1227
128 Leu Ser Thr Arg Ile Gly Ser Gly Ser Phe Gly Thr Val Tyr Lys Gly
129            355               360               365
131 aaa tgg cac gga gat gtt gca gta aag atc cta aag gtt gtc gac cca   1275
132 Lys Trp His Gly Asp Val Ala Val Lys Ile Leu Lys Val Val Asp Pro
133            370               375               380
```

```
135  acc cca gag caa ttc cag gcc ttc agg aat gag gtg gct gtt ctg cgc   1323
136  Thr Pro Glu Gln Phe Gln Ala Phe Arg Asn Glu Val Ala Val Leu Arg
137          385                 390                 395
139  aaa aca cgg cat gtg aac att ctg ctt ttc atg ggg tac atg aca aag   1371
140  Lys Thr Arg His Val Asn Ile Leu Leu Phe Met Gly Tyr Met Thr Lys
141  400                 405                 410
143  gac aac ctg gca att gtg acc cag tgg tgc gag ggc agc agc ctc tac   1419
144  Asp Asn Leu Ala Ile Val Thr Gln Trp Cys Glu Gly Ser Ser Leu Tyr
145  415                 420                 425                 430
147  aaa cac ctg cat gtc cag gag acc aag ttt cag atg ttc cag cta att   1467
148  Lys His Leu His Val Gln Glu Thr Lys Phe Gln Met Phe Gln Leu Ile
149          435                 440                 445
151  gac att gcc cgg cag acg gct cag gga atg gac tat ttg cat gca aag   1515
152  Asp Ile Ala Arg Gln Thr Ala Gln Gly Met Asp Tyr Leu His Ala Lys
153          450                 455                 460
155  aac atc atc cat aga gac atg aaa tcc aac aat ata ttt ctc cat gaa   1563
156  Asn Ile Ile His Arg Asp Met Lys Ser Asn Asn Ile Phe Leu His Glu
157          465                 470                 475
159  ggc tta aca gtg aaa att gga gat ttt ggt ttg gca aca gta aag tca   1611
160  Gly Leu Thr Val Lys Ile Gly Asp Phe Gly Leu Ala Thr Val Lys Ser
161          480                 485                 490
163  cgc tgg agt ggt tct cag cag gtt gaa caa cct act ggc tct gtc ctc   1659
164  Arg Trp Ser Gly Ser Gln Gln Val Glu Gln Pro Thr Gly Ser Val Leu
165  495                 500                 505                 510
167  tgg atg gcc cca gag gtg atc cga atg cag gat aac aac cca ttc agt   1707
168  Trp Met Ala Pro Glu Val Ile Arg Met Gln Asp Asn Asn Pro Phe Ser
169          515                 520                 525
171  ttc cag tcg gat gtc tac tcc tat ggc atc gta ttg tat gaa ctg atg   1755
172  Phe Gln Ser Asp Val Tyr Ser Tyr Gly Ile Val Leu Tyr Glu Leu Met
173          530                 535                 540
175  acg ggg gag ctt cct tat tct cac atc aac aac cga gat cag atc atc   1803
176  Thr Gly Glu Leu Pro Tyr Ser His Ile Asn Asn Arg Asp Gln Ile Ile
177          545                 550                 555
179  ttc atg gtg ggc cga gga tat gcc tcc cca gat ctt agt aag cta tat   1851
180  Phe Met Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Lys Leu Tyr
181  560                 565                 570
183  aag aac tgc ccc aaa gca atg aag agg ctg gta gct gac tgt gtg aag   1899
184  Lys Asn Cys Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys
185  575                 580                 585                 590
187  aaa gta aag gaa gag agg cct ctt ttt ccc cag atc ctg tct tcc att   1947
188  Lys Val Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile
189          595                 600                 605
191  gag ctg ctc caa cac tct cta ccg aag atc aac cgg agc gct tcc gag   1995
192  Glu Leu Leu Gln His Ser Leu Pro Lys Ile Asn Arg Ser Ala Ser Glu
193          610                 615                 620
195  cca tcc ttg cat cgg gca gcc cac act gag gat atc aat gct tgc acg   2043
196  Pro Ser Leu His Arg Ala Ala His Thr Glu Asp Ile Asn Ala Cys Thr
197          625                 630                 635
199  ctg acc acg tcc ccg agg ctg cct gtc ttc tagttgactt tgcacctgtc    2093
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RAW SEQUENCE LISTING   DATE: 08/23/2000
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Input Set : A:\TSR7102.txt
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200  Leu Thr Thr Ser Pro Arg Leu Pro Val Phe
201       640                   645
203  ttcaggctgc caggggagga ggagaagcca gcaggcacca cttttctgct ccctttctcc 2153
205  agaggcagaa cacatgtttt cagagaagct ctgctaagga ccttctagac tgctcacagg 2213
207  gccttaactt catgttgcct tcttttctat ccctttgggc cctgggagaa ggaagccatt 2273
209  tgcagtgctg gtgtgtcctg ctccctcccc acattcccca tgctcaaggc ccagccttct 2333
211  gtagatcgc aagtggatgt tgatggtagt acaaaaagca ggggcccagc cccagctgtt 2393
213  ggctacatga gtatttagag gaagtaaggt agcaggcagt ccagccctga tgtggagaca 2453
215  catgggattt tggaaatcag cttctggagg aatgcatgtc acaggcggga ctttcttcag 2513
217  agagtggtgc agcgccagac attttgcaca taaggcacca aacagcccag gactgccgag 2573
219  actctggccg cccgaaggag cctgctttgg tactatggaa cttttcttag gggacacgtc 2633
221  ctcctttcac agcttctaag gtgtccagtg cattgggatg gtttttccagg caaggcactc 2693
223  ggccaatccg catctcagcc ctctcaggag cagtcttcca tcatgctgaa ttttgtcttc 2753
225  caggagctgc ccctatgggg cgggccgcag ggccagcctg tttctctaac aaacaaacaa 2813
227  acaaacagcc ttgtttctct agtcacatca tgtgtataca aggaagccag gaatacaggt 2873
229  tttcttgatg atttgggttt taattttgtt tttattgcac ctgacaaaat acagttatct 2933
231  gatggtccct caattatgtt attttaataa aataaattaa attt             2977
234  <210> SEQ ID NO: 2
235  <211> LENGTH: 648
236  <212> TYPE: PRT
237  <213> ORGANISM: Homo sapiens
239  <400> SEQUENCE: 2
240  Met Glu His Ile Gln Gly Ala Trp Lys Thr Ile Ser Asn Gly Phe Gly
241   1               5                   10                  15
243  Phe Lys Asp Ala Val Phe Asp Gly Ser Ser Cys Ile Ser Pro Thr Ile
244              20                  25                  30
246  Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly Lys Leu
247          35                  40                  45
249  Thr Asp Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu Pro Asn
250      50                  55                  60
252  Lys Gln Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu His Asp
253  65                  70                  75                  80
255  Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu Cys Cys
256              85                  90                  95
258  Ala Val Phe Arg Leu Leu His Glu His Lys Gly Lys Lys Ala Arg Leu
259              100                 105                 110
261  Asp Trp Asn Thr Asp Ala Ala Ser Leu Ile Gly Glu Glu Leu Gln Val
262          115                 120                 125
264  Asp Phe Leu Asp His Val Pro Leu Thr Thr His Asn Phe Ala Arg Lys
265      130                 135                 140
267  Thr Phe Leu Lys Leu Ala Phe Cys Asp Ile Cys Gln Lys Phe Leu Leu
268  145                 150                 155                 160
270  Asn Gly Phe Arg Cys Gln Thr Cys Gly Tyr Lys Phe His Glu His Cys
271              165                 170                 175
273  Ser Thr Lys Val Pro Thr Met Cys Val Asp Trp Ser Asn Ile Arg Gln
274              180                 185                 190
276  Leu Leu Leu Phe Pro Asn Ser Thr Ile Gly Asp Ser Gly Val Pro Ala
277          195                 200                 205
279  Leu Pro Ser Leu Thr Met Arg Arg Met Arg Glu Ser Val Ser Arg Met
```

```
             RAW SEQUENCE LISTING              DATE: 08/23/2000
             PATENT APPLICATION:  US/09/637,302    TIME: 09:32:54

             Input Set : A:\TSR7102.txt
             Output Set: N:\CRF3\08232000\I637302.raw

280      210                    215                  220
282    Pro Val Ser Ser Gln His Arg Tyr Ser Thr Pro His Ala Phe Thr Phe
283    225                   230                  235                240
285    Asn Thr Ser Ser Pro Ser Ser Glu Gly Ser Leu Ser Gln Arg Gln Arg
286                        245                  250                255
288    Ser Thr Ser Thr Pro Asn Val His Met Val Ser Thr Thr Leu Pro Val
289                   260                  265                270
291    Asp Ser Arg Met Ile Glu Asp Ala Ile Arg Ser His Ser Glu Ser Ala
292                   275                  280                285
294    Ser Pro Ser Ala Leu Ser Ser Ser Pro Asn Asn Leu Ser Pro Thr Gly
295               290                  295                  300
297    Trp Ser Gln Pro Lys Thr Pro Val Pro Ala Gln Arg Glu Arg Ala Pro
298    305                   310                  315                320
300    Val Ser Gly Thr Gln Glu Lys Asn Lys Ile Arg Pro Arg Gly Gln Arg
301                   325                  330                335
303    Asp Ser Ser Tyr Tyr Trp Glu Ile Glu Ala Ser Glu Val Met Leu Ser
304               340                  345                350
306    Thr Arg Ile Gly Ser Gly Ser Phe Gly Thr Val Tyr Lys Gly Lys Trp
307               355                  360                365
309    His Gly Asp Val Ala Val Lys Ile Leu Lys Val Val Asp Pro Thr Pro
310        370                   375                  380
312    Glu Gln Phe Gln Ala Phe Arg Asn Glu Val Ala Val Leu Arg Lys Thr
313    385                   390                  395                400
315    Arg His Val Asn Ile Leu Leu Phe Met Gly Tyr Met Thr Lys Asp Asn
316                   405                  410                415
318    Leu Ala Ile Val Thr Gln Trp Cys Glu Gly Ser Ser Leu Tyr Lys His
319                   420                  425                430
321    Leu His Val Gln Glu Thr Lys Phe Gln Met Phe Gln Leu Ile Asp Ile
322        435                   440                  445
324    Ala Arg Gln Thr Ala Gln Gly Met Asp Tyr Leu His Ala Lys Asn Ile
325    450                   455                  460
327    Ile His Arg Asp Met Lys Ser Asn Asn Ile Phe Leu His Glu Gly Leu
328    465                   470                  475                480
330    Thr Val Lys Ile Gly Asp Phe Gly Leu Ala Thr Val Lys Ser Arg Trp
331                   485                  490                495
333    Ser Gly Ser Gln Gln Val Glu Gln Pro Thr Gly Ser Val Leu Trp Met
334               500                  505                510
336    Ala Pro Glu Val Ile Arg Met Gln Asp Asn Asn Pro Phe Ser Phe Gln
337        515                   520                  525
339    Ser Asp Val Tyr Ser Tyr Gly Ile Val Leu Tyr Glu Leu Met Thr Gly
340        530                   535                  540
342    Glu Leu Pro Tyr Ser His Ile Asn Asn Arg Asp Gln Ile Ile Phe Met
343    545                   550                  555                560
345    Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Lys Leu Tyr Lys Asn
346               565                  570                575
348    Cys Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys Lys Val
349               580                  585                590
351    Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile Glu Leu
352               595                  600                  605
```

Seq # 7

<210> 7
<211> 668
<212> PRT
<213> Artificial Sequence

<400> 7
Met Glu His Ile Gln Gly Ala Trp Lys Thr Ile Ser Asn Gly Phe Gly
 1   5   10   15

*missing mandatory <220> and <223> features to explain artificial sequence. See #12 on Error Summary Sheet. *Also see #7 on Error Summary Sheet*

VERIFICATION SUMMARY   DATE: 08/23/2000
PATENT APPLICATION: US/09/637,302   TIME: 09:32:55

Input Set : A:\TSR7102.txt
Output Set: N:\CRF3\08232000\I637302.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:892 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:892 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: